



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/088,117
Source: PT/10
Date Processed by STIC: 8/14/2002

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- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
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<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
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Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
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Revised 01/29/2002



PCT10

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/088,117

DATE: 08/14/2002
 TIME: 09:31:18

**Does Not Comply
 Corrected Diskette Needed**

Input Set : A:\EP.txt
 Output Set: N:\CRF3\08142002\J088117.raw

3 <110> APPLICANT: CNRS
 5 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES DERIVED FROM GENES CODING FOR
 6 TRIMETHYLAMINE N-OXIDE REDUCTASE, AND USES THEREOF,
 7 ESPECIALLY FOR THE DETECTION OF BACTERIA
 9 <130> FILE REFERENCE: WOB 99 AX CNR DORA
 11 <140> CURRENT APPLICATION NUMBER: US/10/088,117
 12 <141> CURRENT FILING DATE: 2002-07-22
 14 <150> PRIOR APPLICATION NUMBER: FR9911543
 15 <151> PRIOR FILING DATE: 1999-09-15
 17 <160> NUMBER OF SEQ ID NOS: 27
 19 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

823 <210> SEQ ID NO: 27
 824 <211> LENGTH: 17
 825 <212> TYPE: DNA
 826 <213> ORGANISM: Artificial sequence
 828 <220> FEATURE:
 829 <223> OTHER INFORMATION: Description of the artificial sequence:
 830 PCR primer
 832 <400> SEQUENCE: 27
 W--> 833 ttgpcrtcra artgngc
 E--> 836 1
 E--> 838 1

17

VARIABLE LOCATION SUMMARY
PATENT APPLICATION: US/10/088,117

DATE: 08/14/2002
TIME: 09:31:20

Input Set : A:\EP.txt
Output Set: N:\CRF3\08142002\J088117.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:22; N Pos. 9
Seq#:24; N Pos. 3,6
Seq#:27; N Pos. 3,15

8/14/02

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/088,117

DATE: 08/14/2002

TIME: 09:31:20

Input Set : A:\EP.txt

Output Set: N:\CRF3\08142002\J088117.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
 L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:768 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:22
 L:768 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
 L:768 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
 L:794 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
 L:794 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
 L:794 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
 L:833 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:27
 L:833 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
 L:833 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
 L:836 M:254 E: No. of Bases conflict, this line has no nucleotides.
 M:254 Repeated in SeqNo=27

8/14/02